Application No.: 10/006,174

AMENDMENTS TO THE SPECIFICATION:

Please replace paragraph 2 on page 14 with the following amended paragraph:

Microarray can be used in a variety of ways. A preferred microarray contains nucleic acids and is used to analyze nucleic acid samples. Typically, a nucleic acid sample is prepared from appropriate source and labeled with a signal moiety, such as fluorescent label. The sample is hybridized with the array under appropriate conditions. The arrays are washed or otherwise processed to remove non-hybridized sample nucleic acids. The hybridization is evaluated by detecting the distribution of the label on the chip. The distribution of label may be detected by scanning the arrays to determine fluorescence intensity distribution. Typically, the hybridization of each probe is reflected by several pixel intensities. The raw intensity data may be stored in a gray scale pixel intensity file. The GATC^{TM} Consortium has specified several file formats for storing array intensity data. The final software specification is available at the GATC^{TM} Consortium website www.gatcconsortium.org and is incorporated herein by reference in its entirety. The pixel intensity files are usually large. For example, a GATC^{TM} compatible image file may be approximately 50 Mb if there are about 5000 pixels on each of the horizontal and vertical axes and if a two bytes integer is used for every pixel intensity. The pixels may be grouped into cells (see, GATC^{TM} software specification). The probes in a cell are designed to have the same sequence (i.e., each cell is a probe area). A CEL file contains the statistic of a cell, e.g., the 75th percentile and standard deviation of intensities of pixels in a cell. The 50, 60, 70, 75 or 80th percentile of pixel intensity of a cell is often used as the intensity of the cell.

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